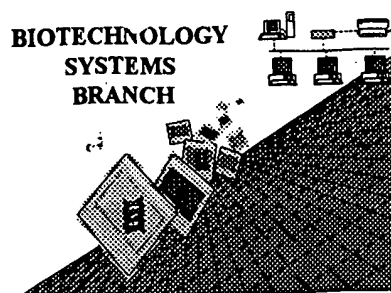


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/814,047  
Source: O/PK  
Date Processed by STIC: 7/25/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/814,047

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/814,047

DATE: 07/25/2001  
TIME: 14:24:43

Input Set : A:\es.txt  
Output Set: N:\CRF3\07252001\I814047.raw

3 <110> APPLICANT: WAKAMATSU, Yuko  
4 OZATO, Kenjiro  
6 <120> TITLE OF INVENTION: SEE-THROUGH MEDAKA  
8 <130> FILE REFERENCE: 04853-0066-00000  
9 <140> CURRENT APPLICATION NUMBER: US/09/814,047  
11 <141> CURRENT FILING DATE: 2001-03-22  
13 <150> PRIOR APPLICATION NUMBER: 09/814,047  
14 <151> PRIOR FILING DATE: 2001-03-22  
16 <160> NUMBER OF SEQ ID NOS: 8  
18 <170> SOFTWARE: PatentIn Ver. 2.0

*delete - these are current  
applications  
Does Not Comply data  
Corrected Diskette Needed*

## ERRORED SEQUENCES

100 <210> SEQ ID NO: 8  
101 <211> LENGTH: 37  
102 <212> TYPE: DNA  
103 <213> ORGANISM: Oryzias latipes  
105 <220> FEATURE:  
106 <223> OTHER INFORMATION: Other information: Primer VP3 used to amplify 5.1 kb genomic  
fragment  
107 comprising the promotor region of vasa gene.  
109 <400> SEQUENCE: 8  
110 agaggatcca atagaatgag taatggttct ctatttc  
E--> 113 (1/5)

*delete*

*see next page*

<210> 3  
<211> 19  
<212> DNA  
<213> Unknown

<220>  
<223> ~~Other information~~ Common sequence found in animals. The sequence is used herein as a forward primer to amplify the short fragment of vasa cDNA.

<400> 3  
atggcgtggyg cncaraqng

19

see item 9 on Eva summary sheet

same eva in seg. 4

## VERIFICATION SUMMARY

DATE: 07/25/2001

PATENT APPLICATION: US/09/814,047

TIME: 14:24:44

Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I814047.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:52 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3  
L:52 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:64 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
L:64 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:113 M:254 E: No. of Bases conflict, LENGTH:Input:5 Counted:38 SEQ:8  
L:113 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:113 M:252 E: No. of Seq. differs, <211>LENGTH:Input:37 Found:38 SEQ:8